

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 31, 2003, 13:11:02 ; Search time 25 Seconds
(without alignments)
989.442 Million cell updates/sec

Title: US-10-082-894-2
Perfect score: 2786
Sequence: 1 MDKYNQVQKVCYLVIDWG.....LMGLPVPPEMDGVPLLEQRG 526

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries.

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1153.5	41.4	515	1	GM11_METAC
2	1151.5	41.3	512	1	GM11_CLOPE
3	1143.5	41.0	510	1	GM11_LISIN
4	1143.5	41.0	521	1	GM12_METAC
5	1141.5	41.0	510	1	GM11_LISMO
6	1127	40.5	510	1	GM11_BACST
7	1124.5	40.4	521	1	GM11_METWA
8	1120	40.2	510	1	GM11_BACHD
9	1118	40.1	510	1	GM11_BACSU
10	1103.5	39.6	511	1	GM11_PACME
11	1088.5	39.1	515	1	GM11_PSEAE
12	1083.5	38.9	510	1	GM11_VIBCH
13	1082	38.8	514	1	GM11_SALTI
14	1078	38.7	533	1	GM11_ANASP
15	1076	38.6	514	1	GM11_SALTY
16	1073.5	38.5	515	1	GM11_YERPE
17	1070.5	38.4	512	1	GM11_OCEIH
18	1067.5	38.3	514	1	GM11_SHEON
19	1065	38.2	510	1	GM11_CLOAB
20	1063	38.2	514	1	GM11_ECOLI
21	1059	38.0	514	1	GM11_ECO57
22	1057	37.9	514	1	GM11_SHIFL
23	1055	37.9	510	1	GM11_PSESM
24	1044.5	37.5	531	1	GM11_SYNEL
25	1023	36.7	508	1	GM11_MYCPN
26	1023	36.7	532	1	GM11_SYNT3
27	999.5	35.9	505	1	GM11_AGRTP5
28	996	35.8	491	1	GM11_HELPY
29	991	35.6	491	1	GM11_HELPJ
30	990.5	35.6	534	1	GM11_PORPU
31	975	35.0	505	1	GM11_STAAM
32	970	34.8	505	1	GM11_STAAN
33	967.5	34.7	508	1	GM11_HALNI

ALIGNMENTS

RESULT 1

ID	GM11_METAC	STANDARD;	PRT;	515 AA.
AC	Q8TWI6:			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1			
DE	(EC 5.4.2.1) (Phosphoglyceromutase 1) (BPG-independent PGAM 1)			
DE	(iPGM 1).			
GN	GMPI1 OR WA2671.			
OS	Methanosarcina acetivorans.			
OC	Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;			
OC	Methanosarcinales; Methanosarcinaceae; Methanosarcina.			
OX	NCBI_TaxID=2214;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C2A / ATCC 33395 / DSM 2834;			
RX	MEDLINE=21929760; PubMed=11932238;			
RA	Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,			
RA	FitzHugh W., Calvo S., Engels R., Smirnov S., Atncor D., Brown A.,			
RA	Allen N., Naylor J., Stange-Thomann N., DeAtellano K., Johnson R.,			
RA	Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,			
RA	Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,			
RA	Hedderich R., Ingram-Smith C., Kuettnar H.C., Krzycki J.A.,			
RA	Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,			
RA	Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,			
RA	Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,			
RA	Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,			
RA	Metcalfe W.W., Birren B.;			
RT	"The genome of Methanosarcina acetivorans reveals extensive metabolic			
RT	and physiological diversity.";			
RL	Genome Res. 12:532-542(2002).			
CC	- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and			
CC	3-phosphoglycerate. (By similarity).			
CC	- CATALYTIC ACTIVITY: 2-phospho-D-glycerate -> 3-phospho-D-glycerate.			
CC	- COFACTOR: Binds 2 manganese ions (By similarity).			
CC	- PATHWAY: Glycolysis.			
CC	- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE			
CC	FAMILY.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; AE010963; AAM05049.1; -			
DR	HMAP; MF 01038; -; 1.			
DR	InterPro; IPR006124; Metalloenzyme.			
DR	InterPro; IPR005995; Pgm_bpd_ind.			
DR	Pfam; PF01676; Metalloenzyme; 1.			
DR	ProDom; PD004429; Pgm_bpd_ind; 1.			
DR	TIGRFAMs; TIGR01307; pgm_bpd_ind; 1.			

Q06464 antithamnio
P47669 mycoplasma
Q9p171 campylobact
Q98qa7 mycoplasma
Q91214 streptomyce
P35494 nicotiana t
Q9m9k1 arabidopsis
Q42908 mesembryant
P35493 ricinus com
P30792 zea mays (m
O04499 arabidopsis
Q9p9w1 ureaplasma

1061.5 34.5 510 1 GPM1_ANTSP
955.5 34.3 507 1 GPM1_MYCME
894.5 32.1 492 1 GPM1_CAMJE
844.5 30.3 505 1 GPM1_MYCFU
749 26.9 511 1 GPM1_STRCO
737 26.5 559 1 PMG1_TOBAC
729 26.2 560 1 PMG2_ARSYH
726 26.1 559 1 PMG1_MESCR
721 25.9 556 1 PMG1_RICCO
720 25.8 559 1 PMG1_MAIZE
706 25.3 557 1 PMG1_ARSYH
699.5 25.1 502 1 GPM1_UREFA

Db 417 AVDECLGKADKVLKEGTFTITADHGNAEVMDISTGKPMHTAHTSDVPFLVWSKDAEG 476
Qy 481 KSTPPTGDDGKERARALRDVAPTVQLMGLPVPPEMDGVPLLEQ 524
Db 477 KSLK---DGK-----LADIAPMLTVNGLEVSEMTGTCLLNK 512

RESULT 3

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GM12_METAC ID GM12_METAC STANDARD; PRT; 510 AA.
AC Q92812; 2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2.3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (1PCM).
GN GPMI OR PGM OR LINP550.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OC NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CLIP 11262 / Serovar 6a;
RA MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluster T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
RA "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -1- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate -> 3-phospho-D-glycerate.
CC -1- COFACTOR: Binds 2 manganese ions (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; AL596172; CAC97777.1; -
DR PIR; A11750; A11750.
DR ListList; LIN02550; -.
DR HANAP; MF_01038; -.
DR InterPro; IPR006124; Metalloenzyme.
DR InterPro; IPR005995; Pgm_bpd_ind.
DR Pfam; PF01676; Metalloenzyme; 1.
DR ProDom; PD004429; Pgm_bpd_ind; 1.
DR TIGRFAMs; TIGR01307; Pgm_bpd_ind; 1.
DR Isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
KW AC_SITE 62 62 PHOSPHOSERINE INTERMEDIATE
FT METAL 12 12 MANGANESE 2 (BY SIMILARITY).
FT METAL 62 62 MANGANESE 2 (BY SIMILARITY).
FT METAL 402 402 MANGANESE 1 (BY SIMILARITY).
FT METAL 406 406 MANGANESE 1 (BY SIMILARITY).
FT METAL 443 443 MANGANESE 2 (BY SIMILARITY).
FT METAL 444 444 MANGANESE 2 (BY SIMILARITY).
FT METAL 461 461 MANGANESE 1 (BY SIMILARITY).
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SQ SEQUENCE 510 AA; 56138 MW; E5AA15A804B16A4D CRC64;
Query Match 41.0%; Score 1143.5; DB 1; Length 510;
Best Local Similarity 44.2%; Pred. No. 3.4e-81;
Matches 231; Conservative 91; Mismatches 174; Indels 27; Gaps 7;
Qy 11 VCLVWIDGWLSDQHGNAIAKAKTPIMDKLCSGNWQ-----KLEAHGLHVLGPEGLMGN 65
Db 6 VAIILIDGFGKRAETVGNVAQANKPNFDY---WANFPHGELKAAGLDVGLPEGQMG 61
Qy 66 SEVGHNLNIGAGRVIIYQDIVINLAVQRNEFFVTPOIVASAEAKKSGSRHLHLGLVSDGG 125
Db 62 SEVGHNLNIGAGRVIIYQSLTRIDKAIEEGEQENKALNNAFTHTKENNSDHLHGLGLSDGG 121
Qy 126 VHSIDHLEFALIRAFKQLOVPKVFIFHFADGRDTSPTSGAGYLEQLLOFTASEKYGLAT 185
Db 122 VHSINHLVALLETAKDKGVKNVYIHFADGRDVAPOSSLEYLETLEKASLDLNYGAIA 181
Qy 186 ITGRYAMORDKRWERIKMAYEAIVGGIGOKATVDKAVDVVVRERYAQOSETDEFUKPIVFS 245
Db 182 VSGRFYAMORDKRWERIKMAYEAIVGGIGOKATVDKAVDVVVRERYAQOSETDEFUKPIVFS 245
Qy 246 DDGR----VKDDDTLFFNVRADMRQICECLGLERYKDLNSSLVPHPKNIQISOMTOYNK 301
Db 240 KDGKPVATVKNDAVIFNFRPDRAIQLSNAFTDKEDWDHFDGNGANFKIKFVMTLYNP 299
Qy 302 EFPFSPFLPPVTHNVLAEMLASOGVTFQCAETEKYPHYTFPPFGGVEQFQDEECMV 361
Db 300 SIDAFAFEPIEMKNVIGEVLSNEGLSQLRIAEETEKYPHYTFPPFGGVEQFQDEECMV 361
Qy 362 PSPEKATYDLKPEMNAAGVAEKVEQIESGRHPLVMCNFAPPDMVGHTGKFEPAKACQ 421
Db 360 NSPK-VETYDLKPEMSAYEVTDAVEDIKNDKHDAIILNANPDMVGHSGMLEPTIKAE 418
Qy 422 ATDEAIGKIFEACOTYNYVLMVTSDHGNAEKMTAPDGESEHTAHTCNLPVPTCSKTFVFK 481
Db 419 AVDENLGRVVDLILEKGSIAIFADHGNSETMSTPEGKPTAHTVTPVIVTKK----- 473
Qy 482 STPTGDDGKERARALRDVAPTVQLMGLPVPPEMDGVPLLEQ 524
Db 474 -----GYTLREGGR-LADVAPTMLDLGLGVKKPAEMTGESLIQK 510
RESULT 4
GM12_METAC ID GM12_METAC STANDARD; PRT; 521 AA.
AC Q8TIY2; 2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2.3-bisphosphoglycerate-independent phosphoglycerate mutase 2
DE (EC 5.4.2.1) (Phosphoglyceromutase 2) (BPG-independent PGAM 2)
DE (1PCM 2).
GN GPM12 OR MA4007.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OC NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RC MEDLINE=21929760; PubMed=11932238;
RX Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Graczyk J.A.,
RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
```

RT The genome of Methanosarcina acetivorans reveals extensive metabolic
RL and physiological diversity.";
CC Genome Res. 12:532-542(2002).
CC -1- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
CC -1- COFACTOR: Binds 2 manganese ions (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY.
CC
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CC
CC EMBL; AE011113; AM07357.1; -
DR HAMAP; MF_01038; -; 1.
DR InterPro; IPR006124; Metalloenzyme.
DR InterPro; IPR005995; Pgm_bpd_ind.
DR Pfam; PF01676; Metalloenzyme; 1.
DR ProDom; PD004429; Pgm_bpd_ind; 1.
DR TIGRFAMs; TIGR01307; Pgm_bpd_ind; 1.
KW Isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
FT ACT_SITE 70 70 PHOSPHOSERINE INTERMEDIATE
FT METAL 20 20 (BY SIMILARITY).
FT METAL 70 70 MANGANESE 2 (BY SIMILARITY).
FT METAL 410 410 MANGANESE 1 (BY SIMILARITY).
FT METAL 414 414 MANGANESE 1 (BY SIMILARITY).
FT METAL 451 451 MANGANESE 2 (BY SIMILARITY).
FT METAL 452 452 MANGANESE 2 (BY SIMILARITY).
FT METAL 470 470 MANGANESE 1 (BY SIMILARITY).
SQ SEQUENCE 521 AA; 57685 MW; 4CF05D68DC211D93 CRC64;
Query Match 41.0%; Score 1143.5; DB 1; Length 521;
Best Local Similarity 45.8%; Pred. No. 3.5e-81;
Matches 242; Conservative 86; Mismatches 167; Indels 33; Gaps 12;
8 QKVCVLVVDGGLSDEQHNIAKAKTIPMDKLSG-NQKLEAHLHVLGPEGLMGNS 66
11 RRLPLMLDGLGVEASEGNAIAETPLNSLLNEFPWCFLECSGEAVGLPEGMGNS 70
67 EVGHLNIGAGRVYQDTRINLSVRNGDFENPVLDSLNSVKNLNDSSLHLMGLVSYGGV 130
71 EVGHLNIGAGRVYQDTRINLSVRNGDFENPVLDSLNSVKNLNDSSLHLMGLVSYGGV 130
127 HSHIDLFLALIRAFKOLQVPKVIHFFADGRDTSPTSGAGYLEQLQIFASEKYGELATI 186
131 HSYMTHLYALIKLRDKGLKLVYIHAFLDGRDVPKALADIRELDAFCCKENGSAIATV 190
187 TGRYVAMDRDKWERIKMAYEALVIGGIGOKATVDKAVDVVRERYAQSTDEFELKP-IVPS 245
191 QGRYVAMDRDKWERIKMAYEALVIGGIGOKATVDKAVDVVRERYAQSTDEFELKP-IVPS 249
246 DGRG-----VKDDDTLFFNYRADRMKRIICECL-----GLERYKDLNSVSPHPKNIQISG 295
250 SDGKPEAVQDNDSTIFFNFRDRAKQLTWAFENDDFDGFPREK-----RPK-VHYVC 301
296 MTOYNKFFPPFLPPVTHTNVLAEWLASQGVTFQHCATEKYPHVTFFPFGNGREVQFOD 355
302 MAQYDETLDLPIAFPPPEELNVLGEVLSKQGLVQLRAETERYAHVTFPLNGQEKCYDG 361
356 EERCWVPSKFEVATYDLRPMNAAGVAEKWQIESGRHPLVNCNFAPPDMVGHGTGKEP 415
362 EDRCLIPSPK-VATYDLRPMNAAGVAEKWQIESGRHPLVNCNFAPPDMVGHGTGKEP 420
416 AVKACQADTEATGKIFECACQTNVYLMVTSIDHNGAEK-IAPDGSSEHTACNLNVPFTCS 474
421 AVQAEVNDVTCVGRITIEALKKAGGVALITADHNGAEQENQHTGEPHTAHTSN--PVRC- 477

QY 475 SKTEVFKSPPTGDDGKERARALRDVAPTVLQMLGVPPEMDGVPLL 522
Db 478 --IYACKGEVKALENGK-----LSDLAPTLDDLGVKPEEMKKGKSLI 518
RESULT 5
GPMI_LISMO STANDARD; PRT; 510 AA.
ID GPMI_LISMO
AC Q8Y4I4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2.3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM; (IPGM).
GN GPMI OR PGM OR LMO2456.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusnick C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouni F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapkat G.,
RA Madoeno E., Maitouren A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlund J., Cossart P.,
RT "Comparative genomics of Listeria species."
RL Science 294:849-852(2001).
CC -1- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
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CC -1- COFACTOR: Binds 2 manganese ions (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY.
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CC
CC EMBL; AL591983; CAD00534.1; -
DR PIR; AH1381; AH1381.
DR ListList; LMO2456; -
DR HAMAP; MF_01038; -; 1.
DR InterPro; IPR006124; Metalloenzyme.
DR InterPro; IPR005995; Pgm_bpd_ind.
DR Pfam; PF01676; Metalloenzyme; 1.
DR ProDom; PD004429; Pgm_bpd_ind; 1.
DR TIGRFAMs; TIGR01307; Pgm_bpd_ind; 1.
KW Isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
FT ACT_SITE 62 62 PHOSPHOSERINE INTERMEDIATE
FT METAL 12. 12 MANGANESE 2 (BY SIMILARITY).
FT METAL 62 62 MANGANESE 2 (BY SIMILARITY).
FT METAL 402 402 MANGANESE 1 (BY SIMILARITY).
FT METAL 406 406 MANGANESE 1 (BY SIMILARITY).
FT METAL 443 443 MANGANESE 2 (BY SIMILARITY).
FT METAL 444 444 MANGANESE 2 (BY SIMILARITY).
FT METAL 461 461 MANGANESE 1 (BY SIMILARITY).
SQ SEQUENCE 510 AA; 56139 MW; 7D282159D9DFCF8 CRC64;

Query Match 41.0%; Score 1141.5; DB 1; Length 510;
 Best Local Similarity 44.0%; Pred. No. 4.8e-81;
 Matches 230; Conservative 92; Mismatches 174; Indels 27; Gaps 7;

QY 11 VCLVVIDGWLSDQHGNAIAKAKTPIMDKLCSGNWQ-----KLEAHLHVLGPEGLMGN 65
 DB 6 VAILIDGFGKRAETVGNNAQAANKPNFDY----WADFPHGEUKAAGLDVGPGEOMGN 61
 QY 66 SEVGHNLNIGAGRVYQDIVRINLAVQORNEFTNPQIVASAEAKKSGRLHLLGLSDGG 125
 DB 62 SEVGHNLNIGAGRVYQSLTRIDKALEEGEFOENKALNNAFTHTKENNSDLHLGSLSDGG 121
 QY 126 VHSIHDLFALIRAFKQLQVPKVFIHFFADGRDTPSGAGYLEQLLOFTASKEYGELAT 185
 DB 122 VHSIHNLVALLETAKDKGVKNVYTHAFDLGRDVAPOSSLEYLETLQKALSIDLNYGAIA 181
 QY 186 ITGRYYANDRKRWRERIKWAYEALVGGIGOKATVDKAVDVVVRERYAQSEWDEELKPIVFS 245
 DB 182 VSGRYANDRKRWRERIKWAYEALVGGIGOKATVDKAVDVVVRERYAQSEWDEELKPIVFS 239
 QY 246 DDGR----VKODDTLFFNYRADRMQRICEGLERYKDLNSSLVPHPKNIQISGMTQYNK 301
 DB 240 KDGKPVATVKONDAVIFENFPRDRAIQLSNAFTDQKWDHDFRGADHPKNIKFVMTLYNP 299
 QY 302 EPPFSLPPVYTHVNLAEWLASGVQTFHCAETKYPHYVTFFFNGREGVQFODEERCWY 361
 DB 300 SIDA EVAPEPIEMKNVIGEVLSNGLSOLRTAETKYPHYVTFFFNMNGRNEEFFGENRILI 359
 QY 362 PSPKEVANYDLKPNNAAGVAEKVQIESGRHPLVNCNAPPDMVGHGTFKFPAYKACQ 421
 DB 360 NSPK-VETVYQPEMSAYEVDALVEDIKNDKDAIILNFANPDMVGHGMLFETRAIE 418
 QY 422 ATDEAIGKIFACQTYNVLVMTSDHGNAEKWIAPDGESEHTAHTCNLVPTCSKTFVFK 481
 DB 419 AVDENLGRVVDLLEKGSALIFADHGNSEMTSPGKPHTAHTVPPVPIVTK-----473
 QY 482 STPTPGDGGKRRARALRDVATPVTLQMLGVLPPMDGVPLEQ 524
 DB 474 -----GVTLREGGR-LADVAPTMLDLGLVKKPAEMTGESLIQK 510

RESULT 6
 GPMI_BACST
 ID GPMI_BACST STANDARD; PRT; 510 AA.
 AC Q9X519;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
 DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (IPGM).
 GN GPMI OR PGM.
 OS Bacillus stearothermophilus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
 OC NCBI_TaxID=1422;
 RN [1]
 RN SEQUENCE FROM N.A., SEQUENCE OF 1-7, AND CHARACTERIZATION.
 RP RP MEDLINE=99318775; PubMed=10388626;
 RX Chander M., Setlow P., Lamani E., Jedrzejas M.J.;
 RA "Structural studies on a 2,3-bisphosphoglycerate independent
 RT phosphoglycerate mutase from bacillus stearothermophilus.";
 RL J. Struct. Biol. 126:156-165(1999).
 RN [2]
 RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS), AND MUTAGENESIS.
 RP RP MEDLINE=20211384; PubMed=10747010;
 RX Jedrzejas M.J., Chander M., Setlow P., Krishnasamy G.;
 RA "Structure and mechanism of action of a novel phosphoglycerate mutase
 RT from Bacillus stearothermophilus.";
 RL EMBO J. 19:1419-1431(2000).
 RN [3]
 RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
 RP RP MEDLINE=20390073; PubMed=10764795;
 RX Jedrzejas M.J., Chander M., Setlow P., Krishnasamy G.;

"Mechanism of catalysis of the cofactor-independent phosphoglycerate mutase from Bacillus stearothermophilus. Crystal structure of the complex with 2-phosphoglycerate.";
 J. Biol. Chem. 275:23146-23153(2000).
 - FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and 3-phosphoglycerate.
 - CATALYTIC ACTIVITY: 2-phospho-D-glycerate -> 3-phospho-D-glycerate.
 - COFACTOR: Binds 2 manganese ions.
 - ENZYME REGULATION: Activity is extremely sensitive to pH.
 - PATHWAY: Glycolysis.
 - SUBUNIT: Monomer.
 - SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE FAMILY.

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 EMBL: AF120091; AAD26328.1; -
 PIR: T46865; T46865.
 PDB: LEUJ; 02-MAR-01.
 PDB: IEQJ; 05-APR-01.
 PDB: 1099; 23-DEC-02.
 HAMAP: MF_01038; -; 1.
 InterPro: IPR006124; Metalloenzyme.
 InterPro: IPR005995; Pgm_bpd_ind.
 Pfam: PF01676; Metalloenzyme; 1.
 ProDom: PD004429; Pgm_bpd_ind; 1.
 TRIGFAMS: TIGR01307; pgm_bpd_ind; 1.
 Trimmerase; Glycolysis; Metal-binding; Manganese; 3D-structure.
 INIT_MET 0 0
 ACT_SITE 61 61 PHOSPHOSERINE INTERMEDIATE.
 METAL 11 11 MANGANESE 2.
 METAL 61 61 MANGANESE 2.
 METAL 402 402 MANGANESE 1.
 METAL 406 406 MANGANESE 1.
 METAL 443 443 MANGANESE 2.
 METAL 444 444 MANGANESE 2.
 METAL 461 461 MANGANESE 1.
 MUTAGEN 11 11 D->N: LOSS OF ACTIVITY.
 MUTAGEN 41 41 H->N: DECREASE IN ACTIVITY.
 MUTAGEN 61 61 S->A: LOSS OF ACTIVITY.
 MUTAGEN 65 65 H->N: STRONG DECREASE IN ACTIVITY.
 MUTAGEN 122 122 H->N: STRONG DECREASE IN ACTIVITY.
 MUTAGEN 124 124 H->N: DECREASE IN ACTIVITY.
 MUTAGEN 127 127 H->N: 5 FOLD DECREASE IN ACTIVITY.
 MUTAGEN 260 260 R->L: LOSS OF ACTIVITY.
 MUTAGEN 406 406 H->N: LOSS OF ACTIVITY.
 MUTAGEN 444 444 H->N: 5 FOLD DECREASE IN ACTIVITY.
 MUTAGEN 461 461 H->N: STRONG DECREASE IN ACTIVITY.
 SEQUENCE 510 AA; 56871 MW; A114F5CEB457BCDE CRC64;

Query Match 40.5%; Score 1127; DB 1; Length 510;
 Best Local Similarity 42.7%; Pred. No. 6.5e-80;
 Matches 224; Conservative 104; Mismatches 169; Indels 28; Gaps 8;

QY 8 QOKVCLVVIDGWLSDQHGNAIAKAKTPIMDKLCSGNWQ-----LEAHLHVLGPEGL 62
 DB 2 KKPVALIILDGFGALRDVETYNNAQAANKPNFDY----WNEYPHHTTLKACGAVGLPEQG 57
 QY 63 MGNSEVGHNLNIGAGRVYQDIVRINLAVQORNEFTNPQIVASAEAKKSGRLHLLGLSV 122
 DB 58 MGNSEVGHNLNIGAGRVYQSLTRINIAIREGEFORNETFLAAMNHVKAQHGTSLSHLFGLS 117
 QY 123 DGGVHSHIDLFLALIRAFKQLQVPKVFIHFFADGRDTPSGAGYLEQLLOFTASEKEYG 182
 DB 118 DGGVHSHIDLFLALIRAFKQLQVPKVFIHFFADGRDTPSGAGYLEQLLOFTASEKEYG 177
 QY 183 LATITGRYYANDRKRWRERIKWAYEALVGGIGOKATVDKAVDVVVRERYAQSEWDEELK 241

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Db 178 IATLSGRYSMDRDRMRDVERKAYRAMVYGE--PTYRDLPLCEIYDSYKHGHIYDEFVLPS 235
QY 242 IVFSDDP---VKDDDTLIFNYRADRMROICECLGLERYKDLNASSVPHPKNIQISGMT 297
Db 236 VIVREDGRPVATIONDAIIFNFPDRDRAIQISNTFTNEDFFRDRGPKPKHFLFFVLIT 295
QY 298 QYNKFFPPSPFPVTHYNVLAEWLASQVTOFHCAETEKYPHVTHFFNGGREGVQFDBE 357
Db 296 HESFTKGVYAFKPTNLDITIGEVLSQHLRQLRIAETEKYPHVTFNFGSGGREGFPCEB 355
QY 358 RCMVSPPEVATYDLKPMNAAGVAEKVQESGRHPLVMCNFAPPDPMVGHGTFEPAY 417
Db 356 RILINSPK-VPTYDLKPEMSAYEVDLALKEADKYDAIILNANPDMVGHSGKLEPTI 414
QY 418 KACQATDAIGKIFACQTYNYVLVSDHGAERKIAPIADGSEHTAHTCNLVPFFCSKT 477
Db 415 KAVEAVEDECLGVDAIILAGGIAITADHNADEVLPDGKQPQTAHTNPNVPVITVTKG 474
QY 478 FVFKSTPTPGDGRKARALRDVAPTVLQMLGLVPPMDGVPL 522
Db 475 IKLR-----DGG-----ILGLDAPTLMLDLGLPQPKEMTKGSLI 508

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RESULT 7

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GPML_METMA
ID GPML_METMA STANDARD; PRT; 521 AA.
AC 08PYF8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (IPGM).
GN GPML OR MM0904.
OS Methanosarcina maezi (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Euryarchaeota orders Incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Goel / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wlezer A., Baeumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boencke M., Steckel S.,
RA Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina maezi: evidence for lateral gene
transfer between Bacteria and Archaea."
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
CC -!- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
CC -!- COFACTOR: Binds 2 manganese ions (By similarity).
CC -!- PATHWAY: Glycolysis
CC -!- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF013316; AAM30600.1; --
CC HAMAP: MF_01038; -- 1.
CC InterPro: IPR006124; Metalloenzyme.
CC DR InterPro: IPR005995; Pgm_bpd_ind.
CC DR Pfam: PF01676; Metalloenzyme; 1.
CC DR ProDom: PD004429; Pgm_bpd_ind; 1.
CC DR TIGRFams: TIGR01307; Pgm_bpd_ind; 1.

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KW Isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
FT ACT_SITE 70 PHOSPHOSERINE INTERMEDIATE
FT METAL 20 20 MANGANESE 2 (BY SIMILARITY).
FT METAL 70 70 MANGANESE 2 (BY SIMILARITY).
FT METAL 410 410 MANGANESE 1 (BY SIMILARITY).
FT METAL 414 414 MANGANESE 2 (BY SIMILARITY).
FT METAL 451 451 MANGANESE 2 (BY SIMILARITY).
FT METAL 452 452 MANGANESE 2 (BY SIMILARITY).
FT METAL 470 470 MANGANESE 1 (BY SIMILARITY).
SQ SEQUENCE 521 AA; 57863 MW; C21EAC4898A023AA CRC64;

Query Match 40.4%; Score 1124.5; DB 1; Length 521;
Best Local Similarity 43.5%; Pred. No. 1e-79;
Matches 233; Conservative 102; Mismatches 158; Indels 43; Gaps 12;

QY 8 QOKVCLVVDGWSLDEQHGNAIAKAKTPIWDKLCSGNWK-----LEAHLHVLGPEG 61
Db 11 RPLMLMDLGDGWEKEEGNAIILAASTPHLDRL-----QKERPSCFLETSGEAVGLPQG 65
QY 62 LMGSEVGHNLGAGRVYQDITRINLAVQRNEFTNPQIVASABRAKKGSRLLHLGLV 121
Db 66 QMGSEVGHNLGAGRVYQDITKINVSIRNGDFENPVLDAISNVKLNSSLHLMGLV 125
QY 122 SDGGVSHIDHLFALIRAFKQLQVPKVEIHFHFAAGROTSPTSGAGYQLQLQFIASEKYG 181
Db 126 SYGGVSHSHMTHLYALIKLAQEKGLKVKYIHVFLDGRDVPVPPKAAALGDVDFACKENQSV 185
QY 182 ELATITGRYAMDRLKRWERTKMAEATVGGIGOKATVDKAVDVVVRERYAQSEDEELKP 241
Db 186 KIATVQGRYAMDRLKRWERTKMAEATVGGIGOKATVDKAVDVVVRERYAQSEDEELKP 244
QY 242 IVFSD-----DGRYKDDDTLIFNYRADRMROICE-----ECLGLERYKDLNASSVPHPKN 290
Db 245 TIVTDSGNPEAVIQDTSIVFLNFRDPRARQLTWAFFVKDDFEGFTRK-----RPK- 296
QY 291 IQISGTOYNKEFFPSPFPVTHYNVLAEWLASQVTOFHCAETEKYPHVTHFFNGGREG 350
Db 297 VHYVCMQAYDETLDLPIAFPPPEELTDVLGKVLSDRGLQLRIAETEKYAHVHTFFLNGGQE 356
QY 351 VOFODEERCWVSPKEVATYDLKPMNAAGVAEKVQESGRHPLVMCNFAPPDPMVGH 410
Db 357 KYCGEDRCLIPSPK-ISTYDLKPEMSAYEYVDEVVKRLLSGKYDVIILNFANMDVGH 415
QY 411 GKFEPAVKACQATDAIGKIFACQTYNYVLVSDHGAERKIAPIADGSEHTAHTCNLY 469
Db 416 GDFEAAVKAVETDNCVGRIVEALRTAGGAALITADHGNABEQMENSHTGEPHTAHTSN-- 473
QY 470 PFTCSSKTFVFKSTPTPGDGRKARALRDVAPTVLQMLGLVPPMDGVPLLEOR 525
Db 474 PVKC---IYTCNGEVKALENGK-----LSDLAPTLLDLLEIPKPEKMTGRSLIVRK 521

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RESULT 8

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GPML_BACHD
ID GPML_BACHD STANDARD; PRT; 510 AA.
AC 09K716;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (IPGM).
GN GPML OR PGM OR BH3557.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;

```


RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RL halodurans and genomic sequence comparison with Bacillus subtilis.";
CC Nucleic Acids Res. 28:4317-4331(2000).
CC -!- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
CC -!- COFACTOR: Binds 2 manganese ions (By similarity).
CC -!- PATHWAY: Glycolysis.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY.
CC
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AP001519; BAB07276.1; -
DR PIR: E84094; E84094.
DR HANAP: MF_01038; -;
DR InterPro: IPR006124; Metalloenzyme.
DR InterPro: IPR005995; Pgm_bpd_ind.
DR Pfam: PF01676; Metalloenzyme; 1.
DR ProDom: PD004429; Pgm_bpd_ind; 1.
DR TIGRFAMs: TIGR01307; Pgm_bpd_ind; 1.
KW isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
FT ACT_SITE 62 62
FT METAL 12 12
FT METAL 62 62
FT METAL 403 403
FT METAL 407 407
FT METAL 444 444
FT METAL 445 445
FT METAL 462 462
SQ SEQUENCE 510 AA; 56453 MW; 52AF47C6E03623E CRC64;
Query Match 40.2%; Score 1120; DB 1; Length 510;
Best Local Similarity 43.0%; Pred. No. 2.3e-79;
Matches 226; Conservative 98; Mismatches 174; Indels 28; Gaps 8;
QY 8 QOKVCLVVDGWSLDEOHGNAIAKAKTPIMDKLCSGNWQK-----LEAHGLHVLGPEGL 62
DB 3 KKPVALIILDFGAMRDEAKGNVAVAKNPNFDY----WNYPHALLKADGEAVGLPEQ 58
QY 63 MGNEVGHNTGAGRVYQDVRINLAVORNEFTVNPQIVASAEARKGSGRLHLLGLVS 122
DB 59 MGNEVGHNTGAGRVYQSLTRVNLSTREGEFFENETFLNANHVKKSGSLHYGLVS 118
QY 123 DGVHSHDHLFALIRAFKQLQVPKVFTHFPADGDRDTSPTSGAGLYEQLLOLFIASEKYE 182
DB 119 DGVHSHDHLFALIRAFKQLQVPKVFTHFPADGDRDTSPTSGAGLYEQLLOLFIASEKYE 178
QY 183 LATITGRYAMDROKRWIRKMAEYVGGIGOKATVDKAVDVVRYVAQSETDFELXP- 241
DB 179 LATLHGRYAMDROKRWIRKMAEYVGGIGOKATVDKAVDVVRYVAQSETDFELXP- 236
QY 242 IVFSDG-----RVKDDDLIFNFYRADRMROICEGLGRLYKDLNSSLVPHPKNTQISGMT 297
DB 237 VITNEDGSPVATIEDDAIIFFNFRPDRAIQMSQVFTNKDFRGDRGKLEKLPQNVYVCLT 296
QY 298 QYNKEFPPLPFPVTHFNLAELASQGVTFHCAETEKEKYPHYTFFFGREGVQFQDE 357
DB 297 HFSETVQGVDAFKPTNLDNTLGEVLAQQNYKQLRIATEKYPHYTFFFGSGREEFPFQEE 356
QY 358 RCMVSPKREYATYDLKPMNAAGVAEKVVEQITSGRHPHVMCNFAPDMVGHGTGKFEAV 417
DB 357 RILDISPK-VATYDLKPMNAEYVTDALNIEADKHVILNLFANPDMVGHSGMLEPTI 415
QY 418 KACQATDEAIGKIFEACQTYNYVLMTVSDHGNAEKMIAPDGSSEHTAHTCNLVPFTCSSKT 477

Db 416 KAVEAVDSCKVVDAILAKGAAVITADHGNADDEVVLEKGPMTAHTNKPVIIVTEEG 475
QY 478 FVFVSTPTGDDGKERARALRDVATVLQMLGLPVPPEMDGVPLLE 523
Db 476 LNLRL-----EDG-----ILADLSPTVLDLLGGKQPAEMTGKTLIK 510
RESULT 9
GPMI_BACSU
ID GPMI_BACSU STANDARD: PRT; 510 AA.
AC P39773; O32250;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (LPGM)
DE (Vegetative protein 107) (VEG107).
GN GPMI OR PGM.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=168 / Marburg;
RX MEDLINE=94292408; PubMed=8021172;
RA Leyva-Vazquez M.A., Setlow P.;
RT "Cloning and nucleotide sequences of the genes encoding triose
RT phosphate isomerase, phosphoglycerate mutase, and enolase from
RT Bacillus subtilis.";
RL J. Bacteriol. 176:3903-3910(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Ghm S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Gulseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Bianchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Iaubert J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Mestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolan C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleicher S., Schroeter R., Scofield F.,
RA Sekiguchi J., Sekowska A., Setor S.J., Serron P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takenaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambut R., Wedler H., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 1-17.
RC STRAIN=168 / IS58;
RX MEDLINE=97443988; PubMed=9298659;
RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
RA Hecker M.;
RT "First steps from a two-dimensional protein index towards a response-


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FT METAL 12 12 MANGANESE 2 (BY SIMILARITY).
FT METAL 62 62 MANGANESE 2 (BY SIMILARITY).
FT METAL 403 403 MANGANESE 1 (BY SIMILARITY).
FT METAL 407 407 MANGANESE 1 (BY SIMILARITY).
FT METAL 444 444 MANGANESE 2 (BY SIMILARITY).
FT METAL 445 445 MANGANESE 2 (BY SIMILARITY).
FT METAL 462 462 MANGANESE 1 (BY SIMILARITY).
FT CONFLICT 225 225 D -> E (IN REF. 2).
SQ SEQUENCE 511 AA; 56563 MW; 7D3FAB449983E6C9 CRC64;

Query Match 39.6%; Score 1103.5; DB 1; Length 511;
Best Local Similarity 43.1%; Pred. No. 4.3e-78;
Matches 227; Conservative 96; Mismatches 175; Indels 29; Gaps 9;

QY 8 QOKVCLVVDGSLDEOHGNAIAKAKTIPMDKLCGNNWOK-----LEAHLGHVGLPEGL 62
Db 3 KKPVALIILDFALRDEKGNVTHAKPNFDRF---WNEYPHATQASAEVGLPEGO 58
QY 63 MGSEVGHNLGTAGRIYQDVRINLAVORNEFTNPQIVASAEKRAKGGRLHLLGLVS 122
Db 59 MGSEVGHNLGTAGRIYQDVRINLAVORNEFTNPQIVASAEKRAKGGRLHLLGLVS 118
QY 123 DGGVSHDHLFALIRAFKQLOVPKVIHFHFDAGDRTSPSTSGAGYLQQLQFIASEKYE 182
Db 119 DGGVSHDHLFALIRAFKQLOVPKVIHFHFDAGDRTSPSTSGAGYLQQLQFIASEKYE 178
QY 183 LATITGRYAMDRKRWERIKWAYEAIYGGIGOKATVDKAVDVVVRERYAQSETEFLKP- 241
Db 179 IATISGRYAMDRKRWERIKWAYEAIYGGIGOKATVDKAVDVVVRERYAQSETEFLKP- 236
QY 242 IVFSDDG----RVKDDDTLTFNRYADRMROICELGLERYKLNLSVPPHKNQIQISGMT 297
Db 237 VITKEDGSPVATIQEDAVIFNFRPDRAIQISNTEANEDFRSFDREKHPKHLHFVCLT 296
QY 298 QYNKEFPSPFLPPVTHNVLAEWLASGVYQFHCATEKYPHYTFFNGREVRQODEE 357
Db 297 HFSEVTDGVYAFKPINLDTNLGEVLSQNNKQLRAETEKYPHYTFFNGREVRQODEE 356
QY 358 RCWVPSKPEVATYDLKPMNNAAGVAEKVQIESGRHPLVNCNFPDPMDVGHGCKFEPAV 417
Db 357 RILIDSPK-VATYDLKPMNNAAGVAEKVQIESGRHPLVNCNFPDPMDVGHGCKFEPAV 415
QY 418 KACQATDRAIKIFEACQTYNYVLMVTSDHGNKEMKIAPDGSHTAHTCNLVPFTCSKST 477
Db 416 KAIETVDECLGKIVDAILAKGTAITADHGNADAVITLGNMTAHTNPVP-----V 469
QY 478 FVFKSTPTGDDGKERARALDVAFTVLQ-LMGLVPVPMGVLLLE 523
Db 470 IVTKOGLEREDG-----ILGDLAPTMLTFLDVAQPKEMTGKTLIK 511
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RESULT 11
GPMI_PSEAE
ID GPMI_PSEAE STANDARD; PRT; 515 AA.
AC Q9HU53;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (IPGM).
GN GPMI OR PCM OR PA5131.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
SEQUENCE FROM N.A.A.
RC STRAIN-ATCC 15692 / PAOI;
RX MEDLINE=2043737; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Huynh W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
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RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RA opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -1- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate -> 3-phospho-D-glycerate.
CC -1- COFACTOR: Binds 2 manganese ions (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; AE004926; AAC08516.1; -.
DR HAMAP; MF_01038; -.
DR InterPro; IPR006124; Metalloenzyme.
DR InterPro; IPR005995; Pgm_bpd_ind.
DR Pfam; PF01676; Metalloenzyme; 1.
DR ProDom; PD004429; Pgm_bpd_ind; 1.
DR TIGRFAMs; TIGR01307; Pgm_bpd_ind; 1.
KW Isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
FT ACT_SITE 64 64
FT METAL 14 14 MANGANESE 2 (BY SIMILARITY).
FT METAL 64 64 MANGANESE 2 (BY SIMILARITY).
FT METAL 404 404 MANGANESE 1 (BY SIMILARITY).
FT METAL 408 408 MANGANESE 1 (BY SIMILARITY).
FT METAL 445 445 MANGANESE 2 (BY SIMILARITY).
FT METAL 446 446 MANGANESE 2 (BY SIMILARITY).
FT METAL 464 464 MANGANESE 1 (BY SIMILARITY).
SQ SEQUENCE 515 AA; 55601 MW; AC8C4404189BEC7 CRC64;

Query Match 39.1%; Score 1088.5; DB 1; Length 515;
Best Local Similarity 45.0%; Pred. No. 6.4e-77;
Matches 232; Conservative 78; Mismatches 180; Indels 25; Gaps 9;

QY 13 LVVIDGWLSDQEHGNAIAKAKTIPMDKLCGNNWOKL-EAHLGHVGLPEGLMNGSEVGH 71
Db 10 LIIDGFGHSDSPDYNATYAAKPVMDRLATQPHGLISGSGMDVGLPDGQMGSEVGH 69
QY 72 NIGAGRVYQDVRINLAVORNEFTNPQIVASAEKRAKGGRLHLLGLVSDGGVHSHID 131
Db 70 NLGAGRVYQDVRTRVTKAIRDGEFFENPVIAAGVDKAVAAKAVHILGLLSPGCVHSHED 129
QY 132 HLFALIRAFKQLOVPKVIHFHFDAGDRTSPSTSGAGYLEQLQFIASEKYGELATIGRY 191
Db 130 HLVAQAQMAARRAGAGKIYHAFDLGRDTPPKSAQPSLERLDATFAGLKGRIASTIGRY 189
QY 192 AMDRDKRWERTKMAEYEAIVGGIGOKATVDKAVDVVVRERYAQSETEFLKPIVSDDG--- 248
Db 190 AMDRDNWRDVRQAAAYELIIVDGKAE-FTADSSDALEAAYARGESDEFKATAVVPAGAE 248
QY 249 -RVKDDDTLTFNRYADRMROICELGLERYKLNLSVPPHKNQIQISQ---MTOYNKEFP 304
Db 249 VRVEDGDAVFPMFRADRLARELSRAVPEAFNEF---PRRAPHQLAGVMTQTAAIP 304
QY 305 PPSLFPVPTHTNVLAEWLASGVYQFHCATEKYPHYTFFNGREVRQODEERQWVSP 364
Db 305 APCAFPEPLTNVLGEYLAKHGKQLRAETEKYAHVYTFPFGSGREEPEGEERILITSP 364
QY 365 KEVATYDLKPMNNAAGVAEKVQIESGRHPLVNCNFPDPMDVGHGCKFEPAVKACQATD 424
Db 365 K-VATYDLQPEMSAPEVTDRIATEIQOQRYDVIVVNYANGMDVGHGTVGFEAAVKAECVLD 423
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FT	METAL	461	461	MANCANESE 1 (BY SIMILARITY).
5Q	SEQUENCE	510 AA;	55364 MW;	0607A64DA6DD955B CRC64;
	Query Match	38.9%;	Score 1083.5;	DB 1; Length 510;
	Best Local Similarity	43.1%;	Pred. No. 1.5e-76;	
	Matches	226;	Conservative	87; Mismatches 180; Indels 31; Gaps 10;
Qy		6	NVQKVCLVVDGWLSDQHGNAIAKATPI	MDKLCSGNWOKL-EAHGLHVGLPEGLMG 64
			::: ::	::: ::
Db		2	SAKKPMALVLDGGYREDNANNANINAR	PTVMDSLMANNPHPTLISASGMDVGLDQGMG 61
			::: ::	::: ::
Qy		65	NSEVGHINIGAGRIYQDIIVRINLAVOR	NFVNQIVASAEAKKSGRLHLGLVSDG 124
			::: ::	::: ::
Db		62	NSEVGHINIGAGRIYQDLTRITKAIMDGE	FQHNKVLVAADKAVAKGAVHLMGLSPG 121
			::: ::	::: ::
Qy		125	GVHSHDHLFALIRAFKOLQVPKVFIRH	FADGRDTSPTSGAGYLEQLQLTIASEKYGELA 184
			::: ::	::: ::
Db		122	GVHSHEDIIVAAVEMAAARGAEKTYLH	CFDLGRDTPPRSASLKRQDLFAKLGKGRIA 181
			::: ::	::: ::
Qy		185	TIITGRVYAMDQDKWERIKMAYEALVGG	IGQKATVDKAVDVVRERYAQSETDEFLKPIVF 244
			::: ::	::: ::
Db		182	SIVGRVYAMDQDNNDWVRKAYADLLT	LAQGE-FTYDSAVEALQAAAYAREENDEVFKATEI 240
			::: ::	::: ::
Qy		245	SDDGR-----VKDDTLFFNYRADRM	RQIC-----ECILGLERYKDLANSVPHKNIQISG 295
			::: ::	::: ::
Db		241	RAAGQESAAAGDGDALLFMVYRADRA	RQITRTFVPDFAGFSR-----KAFP-----ALDFVM 292
			::: ::	::: ::
Qy		296	MTQYNKEFPSPSLFPPVTHYNVLAEWL	ASGVQTFHCATEKYPHYVTFPFGNGREVQFOD 355
			::: ::	::: ::
Db		293	LTQYAADIPLOCAFPGPASLENTYGEW	LSKAGKTQLRISETTEKYAHVTFPFGNGVENEFPFG 352
			::: ::	::: ::
Qy		356	EERCMPSPKEVATYDLKPEWNAAGVAK	EVQEQTESGRHPLVMCNFAPPDMVGHGTGKFEP 415
			::: ::	::: ::
Db		353	EEERQVASPK-VATYDLOPEMSSKELT	DKLVAALKSKGYDALICNYPNGMDVGHGTGYVEA 411
			::: ::	::: ::
Qy		416	AVRACQATDEAIGKIFRACQTYNVLM	VTSDHGNAEKMIAPD-GSEHTAHTCNLVPTPCS 474
			::: ::	::: ::
Db		412	AVKRAEAVDCIGRWVAIRKEVDGQLL	TADHAGNAEMMIDPETGGVHTAHTSLPVPL--- 468
			::: ::	::: ::
Qy		475	SKTFVFKSTPTPGDGRERARALRDVAP	TVLQMLGLPVPVPMGDG 518
			::: ::	::: ::
Db		469	--IYVGNKATSLKEGGK-----LSD	LAPTMLALSDLDIPADMSG 505
			::: ::	::: ::
RESULT 13				
GPMLI_SALTI				
ID	GPMLI_SALTI	STANDARD;	PRT;	514 AA.
AC	Q82F0;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	2.3-bisphosphoglycerate-independent phosphoglycerate mutase			
DE	(EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (IPGM).			
GN	GPMI OR STY4091 OR T3815.			
OS	Salmonella typhi.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Salmonella.			
OX	NCBI_TaxID=601;			
ON	[1]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=Ct18.			
RX	MEDLINE=21534947; PubMed=11677608;			
RA	Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,			
RA	Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,			
RA	Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,			
RA	Cronin A., Davis P., Davies R.M., Dowd L., White N., Farfar J.,			
RA	Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,			
RA	Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,			
RA	Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,			
RA	Whitehead S., Barrall B.G.;			
RT	*Complete genome sequence of a multiple drug resistant Salmonella			
RL	Nature 413:848-852(2001).			
RL	NT			

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RN RP SEQUENCE FROM N.A.
RC STRAIN-Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyonanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and Cr18."
RL J. Bacteriol. 185:2330-2337(2003).
CC -1- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
CC -1- COFACTOR: Binds 2 manganese ions (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY.
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CC EMBL; AL627280; CAD03290.1; ALT_INIT.
CC EMBL; AE016847; AA071297.1; ALT_INIT.
CC HAMAP; MF_01038; -.
CC InterPro; IPR006124; Metalloenzyme.
CC InterPro; IPR005995; Pgm_bpd_ind.
CC Pfam; PF01676; Metalloenzyme; 1.
CC ProDom; PD004429; Pgm_bpd_ind; 1.
CC TIGRfam; TIGR01307; Pgm_bpd_ind; 1.
KW Isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
FT ACT_SITE 64
FT METAL 14
FT METAL 64
FT METAL 403
FT METAL 407
FT METAL 444
FT METAL 445
FT METAL 463
SQ SEQUENCE 514 AA; 56312 MW; 48E8D203AABE3D34 CRC64;

Query Match 38.8%; Score 1082; DB 1; Length 514;
Best Local Similarity 42.1%; Pred. No. 2e-76;
Matches 223; Conservative 96; Mismatches 171; Indels 40; Gaps 10;

QY 8 QOKVCLVVDGWLSDQHGNAIAKATPIMDKLCSGNWOK-----LEAHLHVLPEGL 62
DB 5 KKPWLVILDGTYGTEQDQDINAKTPVMDAL----WAKRPTLIDASGLEVLGPDQR 60

QY 63 MGNSEVGHNLGAGRIYQDVRINLAVORNEFTNPOIVASAEARKKSGRLHLGLVS 122
DB 61 MGNSEVGHNLGAGRIYQDRLDVEIKETTFANPVLTVNAVQAKNAGKAVHMGILLS 120

QY 123 DGGVHSHDHLFALIRAFKQLQVVFHFHFDAGDRDTPSPTSGAGYLEQLLOFIASEKYE 182
DB 121 AGGVHSHEDHTTMAAEEAERGAEKIYILHAFLDGRDTPPRSAAELSKFKEDFAALGKGR 180

QY 183 LATITGRYYAMDRKWRERIKWAYEIVGGIGQKATVDKAVDVVVRERYAQSEDEFKLP 242
DB 181 VASIVGRYYAMDRNRWRDVEKAYDLMTLAGOE-FQADTAVAGQAAYARDENDEFVKAT 239

QY 243 VFSDGDR-----VKDDDTLFFNYRADRMROIQCECL-----GLERYKDLNLSVPHPKNIQ 292
DB 240 VIRAEQGADAAMEDGDTLFFNFRADRAREITRAFVNADFDGFAKKV-----NLN 291

QY 293 ISGMTQYNKEPPFPPLPPVTHTVLAEWLASQGVQTPHCAETKYPHVTFFFNGREYQ 352
DB 292 FVMLTEVAADIKTAVAYPPASLANFTGEWMAKNDKTLQRISETEKYAHVTFFFNGVVEP 351

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QY 353 FQDERCMVSPKEVATYDLKPEMNAAGVAEKVQEIESGRHPLVMCMCNEAPPDMVGTGK 412
DB 352 FAGEERILINSPK-VATYDLOPEMSSAELEKLVAAIESGYDTIICNPNGDMVGHGV 410
QY 413 FEPAVKACQATDEAIGKIFACQTYNYVLVMTSDHGNAEKMIAP-DGSEHTAHTCNLVPE 471
DB 411 MEAAIKAVCALDNCIEQVTRAVESVGGOLLITADHGNAEQMRDPATGOEHTAHTNLPVL 470
QY 472 TCSKSTFFVFKSTPTPTGDDGKERARALRDVAPTQLMGLPVPPEMDGVPL 521
DB 471 -----IYVGEKNVKAEGGK-----LSDIAPTMLSLMGMEIPEQMTGKPL 510

RESULT 14
GPMI_ANASP STANDARD; PRT; 533 AA.
ID GPMI_ANASP
AC OBYPL2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (iPGM).
GN GPMI OR ALL4182.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriquchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
CC -1- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
CC -1- COFACTOR: Binds 2 manganese ions (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY.
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CC PIR; AG2328; AG2328.
CC HAMAP; MF_01038; 1.
CC InterPro; IPR006124; Metalloenzyme.
CC InterPro; IPR005995; Pgm_bpd_ind.
CC Pfam; PF01676; Metalloenzyme; 1.
CC ProDom; PD004429; Pgm_bpd_ind; 1.
CC TIGRfam; TIGR01307; Pgm_bpd_ind; 1.
KW Isomerase; Glycolysis; Metal-binding; Manganese; Complete proteome.
FT ACT_SITE 65
FT METAL 15
FT METAL 65
FT METAL 398
FT METAL 402
FT METAL 439
FT METAL 440
FT METAL 457

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